

1/21
FcR-I

1	GCAGGAATTCGGCACGAGCCTCTGTCCTGCCAGCACCGAGGGCTCATCCATCCACAGAGC	60
61	AGTGCAGTGGGAGGAGACGCCATGACCCCCATCCTCACGGTCCTGATCTGTCTCGGGCCC	120
1	<u>M T P I L T V L I C L G P</u>	13
121	CTCCCCAAGCCCACCCTCTGGGCTGAGCCAGGCTCTGTGATCACCCAAGGGAGTCCTGTG	180
14	<u>L P K P T L W A E P G S V I T Q G S P V</u>	33
181	ACCCTCAGGTGTCAGGGGAGCCTGGAGACGCAGGAGTACCATCTATATAGAGAAAAGAAA	240
34	T L R C Q G S L E T Q E Y H L Y R E K K	53
241	ACAGCACTCTGGATTACACGGATCCACAGGAGCTTGTGAAGAAGGGCCAGTTCQQCATC	300
54	T A L W I T R I P Q E L V K K G Q F P I	73
301	CTATCCATCACCTGGGAACATGCAGGGCGGTATTGCTGTATCTATGGCAGCCACACTGCA	360
74	L S I T W E H A G R Y C C I Y G S H T A	93
361	GGCCTCTCAGAGAGCAGTGACCCCCTGGAGCTGGTGGTGACAGGAGCCTACAGCAAACCC	420
94	G L S E S S D P L E L V V T G A Y S K P	113
421	ACCCTCTCAGCTCTGCCCAGCCCTGTGGTGACCTCAGGAGGGAATGTGACCATCCAGTGT	480
114	T L S A L P S P V V T S G G N V T I Q C	133
481	GACTCACAGGTGGCATTGTGATGGCTTCATTCTGTGTAAGGAAGGAGAAGATGAACACCCA	540
134	D S Q V A F D G F I L C K E G E D E H P	153
541	CAATGCCTGAACCTCCATTCCCATGCCCCGTGGGTGCATCCCGGGCCATCTTCTCCGTGGGC	600
154	Q C L N S H S H A R G S S R A I F S V G	173
601	CCCGTGAGCCCCAAGTCGCAGGTGGTTCGTACAGGTGCTATGGTTATGACTCGCGCTCCC	660
174	P V S P S R R W S Y R C Y G Y D S R A P	193
661	TATGTGTGGTCTCTACCCAGTGATCTCCTGGGGCTCCTGGTCCCAGGTGTTTCTAAGAAG	720
194	Y V W S L P S D L L G L L V P G V S K K	213
721	CCATCACTCTCAGTGCAGCCGGGTCTGTCGTGGCCCCCTGGGGAGAAGCTGACCTTCCAG	780

FIG. 1A

2/21

FcR-I

214	P S L S V Q P G P V V A P G E K L T F Q	233
781	TGTGGCTCTGATGCCGGCTACGACAGATTGTCTGTACAAGGAGTGGGGACGTGACTTC	840
234	C G S D A G Y D R F V L Y K E W G R D F	253
841	CTCCAGCGCCCTGGCCGGCAGCCCCAGGCTGGGCTCTCCCAGGCCAACTTCACCCTGGGC	900
254	L Q R P G R Q P Q A G L S Q A N F T L G	273
901	CCTGTGAGCCGCTCCTACGGGGGCCAGTACACATGCTCCGGTGCATACAACCTCTCCTCC	960
274	P V S R S Y G G Q Y T C S G A Y N L S S	293
961	GAGTGGTCGGCCCCCAGCGACCCCTGGACATCCTGATCACAGGACAGATCCGTGCCAGA	1020
294	E W S A P S D P L D I L I T G Q I R A R	313
1021	CCCTTCCTCTCCGTGCGGCCGGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCTGCTG	1080
314	P F L S V R P G P T V A S G E N V T L L	333
1081	TGTCAGTCACAGGGAGGGATGCACACTTTCTTTTGACCAAGGAGGGGGCAGCTGATTCC	1140
334	C Q S Q G G M H T F L L T K E G A A D S	353
1141	CCGCTGCGTCTAAATCAAAGCGCCAATCTCATAAGTACCAGGCTGAATTCCCCATGAGT	1200
354	P L R L K S K R Q S H K Y Q A E F P M S	373
1201	CCTGTGACCTCGGCCCACGCGGGGACCTACAGGTGCTACGGCTCACTCAGCTCCAACCCC	1260
374	P V T S A H A G T Y R C Y G S L S S N P	393
1261	TACCTGCTGACTACCCCAGTGACCCCCTGGAGCTCGTGGTCTCAGGAGCAGCTGAGACC	1320
394	Y L L T H P S D P L E L V V S G A A E T	413
1321	CTCAGCCCACCACAAAACAAGTCCGACTCCAAGGCTGGTGAGTGAGGAGATGCTTGCCGT	1380
414	L S P P Q N K S D S K A G E *	427
1381	GATGACGCTGGGCACAGAGGGTCAGGTCCTGTCAAGAGGAGCTGGGTGTCCTGGGTGGAC	1440
1441	ATTTGAAGAATTATATTCAATTCCAAGTGAAGAATTATTCAACACCTTTAACAATGTATA	1500
1501	TGTGAAGTACTTTATTCTTTCATATTTTAAAAATAAAAGATAATTATCCATG	1552

FIG. 1B

3/21

Percent Similarity: 63.090

Percent Identity: 45.064

HMQD020.aa x FCg2RBos.aa

191 RPYVWSLPSDLLGLLVPGVSKKPSLSVQGPVVPAGEKLTFCGSDAGY 240

[illegible]

6 PALLCLGLSVGLRTQVQAGTFPKPIIWAEPSSVVPLGSSVTILCQGPPNT 55

241 DRFVLYKEWGRDFLQRPGRQPQAGLSQANFTLGPVSRSYGGQYTCSGAYN 290

.. | | | | | : : . . . : . | | | : : | . : | . | | .

56 KSFSLNKE..GDSTPWNHPSLEPWDKANFFISNVREQQAGRYHCS..HF 101

291 LSSEWSAPSDPLDILITGQ.....IRARPFLSVRPGPTVASGENVTLLCQ 335

[illegible]

102 IGVNWSEPSEPLDLLVAGEEPAGRLRDRPSLSVRPSPSVAPGENVTLLCQ 151

336 SQGGMHTFLTKEGAADSPRLKSKRQSHKYQAEFPMSPV TSAHAGTYRC 385

||.. .|||.||||.|..|||.|:|. .|. .|||.|.:|||.|:|

152 SGNRTDTFLLSKEGAHRPLRLRSQDQDGWYQAEFSLSPV TSAHG G TYRC 201

386 YGSLSSNPYLLTHPSDPLELVVSG.....AAETL.....SP 416

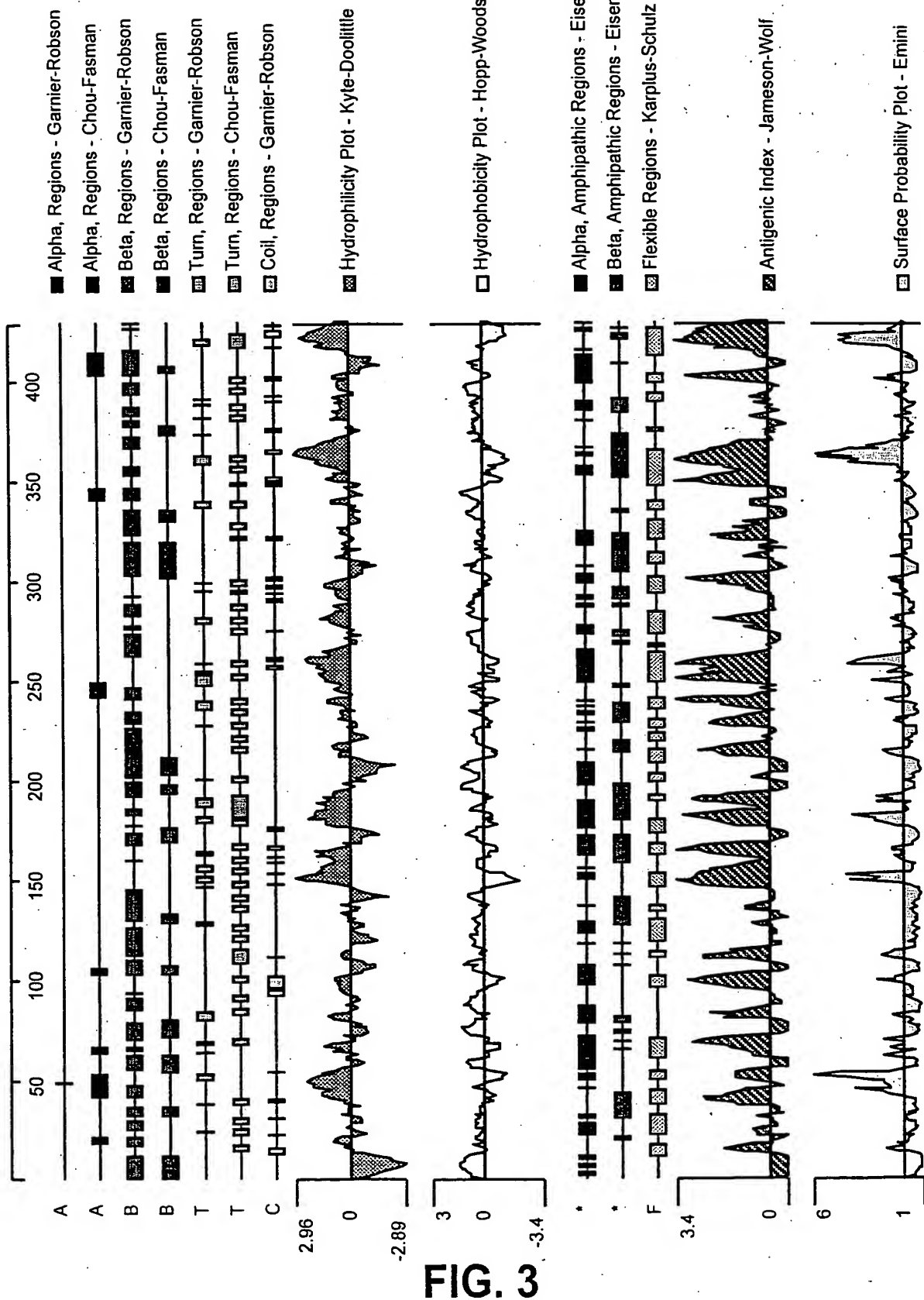
$\frac{1}{2} \cdot \frac{1}{2} = \frac{1}{4}$

202 YRSLSTNPYLLSQPSEPLALLVADYTMQNLRMGLAASVLLLLGILLCQA 251

417 PQNKSDSKAGE 427

252 RHDHGGAREAA 262

FIG. 2



5/21

FcRII

1	ACCCACGCGTCCGCACTCTAGCGGTATCTGCCCACCATGGCCCTGGTGCTGATCCTCCAG	60
1	<u>M A L V L I L Q</u>	8
61	CTGCTGACCCTCTGGCCTCTGTGTACACAGACATCACTCCGTCTGTCCCCCAGCTTCA	120
9	<u>L L T L W P L C H T</u> D I T P S V P P A S	28
121	TACCACCCTAAGCCATGGCTGGGAGCTCAGCCGGCTACAGTTGTGACCCCTGGGGTCAAC	180
29	Y H P K P W L G A Q P A T V V T P G V N	48
181	GTGACCTTGAGATGCCGGGCACCCCAACCCGCTTGGAGATTTGGA CTTTCAAGCCTGGA	240
49	V T L R C R A P Q P A W R F G L F K P G	68
241	GAGATCGCTCCCCTTCTCTCCGGGATGTGTCTCCGAGCTGGCAGAATTCTTTCTGGAG	300
69	E I A P L L F R D V S S E L A E F F L E	88
301	GAGGTGACTCCAGCCCAAGGGGGAAGTTACCGCTGCTGCTACCGAAGGCCAGACTGGGGG	360
89	E V T P A Q G G S Y R C C Y R R P D W G	108
361	CCGGGTGTCTGGTCCCAGCCCAGCGATGTCTGGAGCTGCTGGTGACAGAGGAGCTGCCG	420
109	P G V W S Q P S D V L E L L V T E E L P	128
421	CGGCCGTCGCTGGTGGCGCTGCCCCGGGCCGGTGGTGGTCCTGGCGCCAACGTGAGCCTG	480
129	R P S L V A L P G P V V G P G A N V S L	148
481	CGCTGCGCGGGCCGCTGCGGAACATGAGCTTCGTGCTGTACCGCGAGGGCGTGGCGGCC	540
149	R C A G R L R N M S F V L Y R E G V A A	168
541	CCGCTGCAGTACCGCCACTCCGCGCAGCCCTGGGCGGACTTCACGCTGCTGGGCGCCCGC	600
169	P L Q Y R H S A Q P W A D F T L L G A R	188
601	GCCCCGGGCACCTACAGCTGTACTATCACAGCCCTCCGCGCCCTACGTGCTGTGCGCAG	660
189	A P G T Y S C Y Y H T P S A P Y V L S Q	208

FIG. 4A

6/21

FcRII

661 CGCAGCGAGGTGCTGGTCATCAGCTGGGAAGACTCTGGCTCCTCCGACTACACCCGGGGG 720
209 R S E V L V I S W E D S G S S D Y T R G 228
721 AACCTAGTCCGCCTGGGGCTGGCCGGGCTGGTCCTCATCTCCCTGGGCGCGCTGGTCACT 780
229 N L V R L G L A G L V L I S L G A L V T 248
781 TTTGACTGGCGCAGTCAGAACCGCGCTCCTGCTGGTATCCGCCCTGAGCCCCAGGAGCA 840
249 F D W R S Q N R A P A G I R P * 263
841 CTGCAGCCCCGAGACTTCCAACCTGAGTGGCGGAGAAGCTGGGACCCTGGGCTGGACTGTC 900
901 CTTTCCTGCAGCCCCACAGTCCTGCTGGCTGAGCTCCGCGGAACGGTCCTTAGACCCCGC 960
961 TGTGCCCTGTGCTGTAGCTTCTTTCCAGGCCTTTCCAAGGAGTAGCTGAAAGGAAGACG 1020
1021 CGATTAGTGGTTAAGACTTCCAAGCCAGAAGACAGAGGGTTCGAATCCCAGCACTGCCGT 1080
1081 CTACTCACTGTAGTAGTAGCAGCTACAGAAAGGTAGTAGTGAGACGTGAAGCCAGCTGGA 1140
1141 CTTCTGGGTTGAATGGGGACCTGGAGAACTTTCTGTCTTACAAGAGGATTGTAAATG 1200
1201 GACCAATCAGCACTCTGTAAGATGGACCAATCAGCGCTCTGTAAAATGGACCAATCAGCA 1260
1261 GGACATGGGCGGGGACAATAAGGGAATAAAAGCTGGCGAGCGGGCACCCACCAGAGTC 1320
1321 TGCTTCCAGCTGTGGGAGCTTTGTTCTCTTGCTCTACACAATAAATCTTGCTGCTGCTA 1380
1381 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1410

FIG. 4B

7/21

Percent Similarity: 54.400

Percent Identity: 37.600

HDPMK33.aa x FCg2RBos.aa

5 LILQLLTLWPLCHTDITPSVPPASYHPKPWLGAQPATVVTPGVNVTLCR 54
: | .|:.||: ||| : |:|..||. | .||: |.
1 MAPTLPALCLGLSVGLRTQVQAGTFPKPIIWAEPSSVVPLGSSVTILCQ 50
55 APQPAWRFGFLFKPGEIAPLLFRDV..SSELAEFFLEEVTPAQGGSYRCCY 102
:|. ...|:| |. |: .|: ::. ... |:|:|:| ..|:|. |:|:
51 GPPNTKSFSLNKEGDSTPWNHPSLEPWDKANFFISNVREQQAGRYHCS. 99
103 RRPDWGPGVWSQPSDVLELLVTEELP.....RPSLVALPGPVVGPGANV 146
.: .. ||:|:|:|:|:|:| | | | | . |:| |:|:|:|
100 ...HFIGVNWSEPSEPLDLLVAGEEPAGRLRDRPSLSVRPSPSVAPGENV 146
147 SLRCAGRLRNMSFVLYREGVAA.PLQYRHSAP...WADFTL..LGARAP 190
.| |:| |. |:| :|:| | |..| |. |:| | :...
147 TLLCQSGNRTDTFLLSKEGAHRPLRLRSQDQDGWYQAEFSLSPVTSAHG 196
191 GTYSCYYHTPSAPYVLSQRSEVLVISWEDSGSSDYTRGNLVRLGLAGLVL 240
|||.|| ...||:|:|:|:|:|:| .|||..||:|:|:|:| ||
197 GTYRCYRSLSTNPYLLSQPSEPLALL.....VADYTMQNLIRMGLAASVL 241
241 ISLGALVTFDWRSQNRAPAGIRP 263
: || |: . :.: . . |: : |.
242 LLLGILLCQARHDHGGAREAAARS 264

FIG. 5

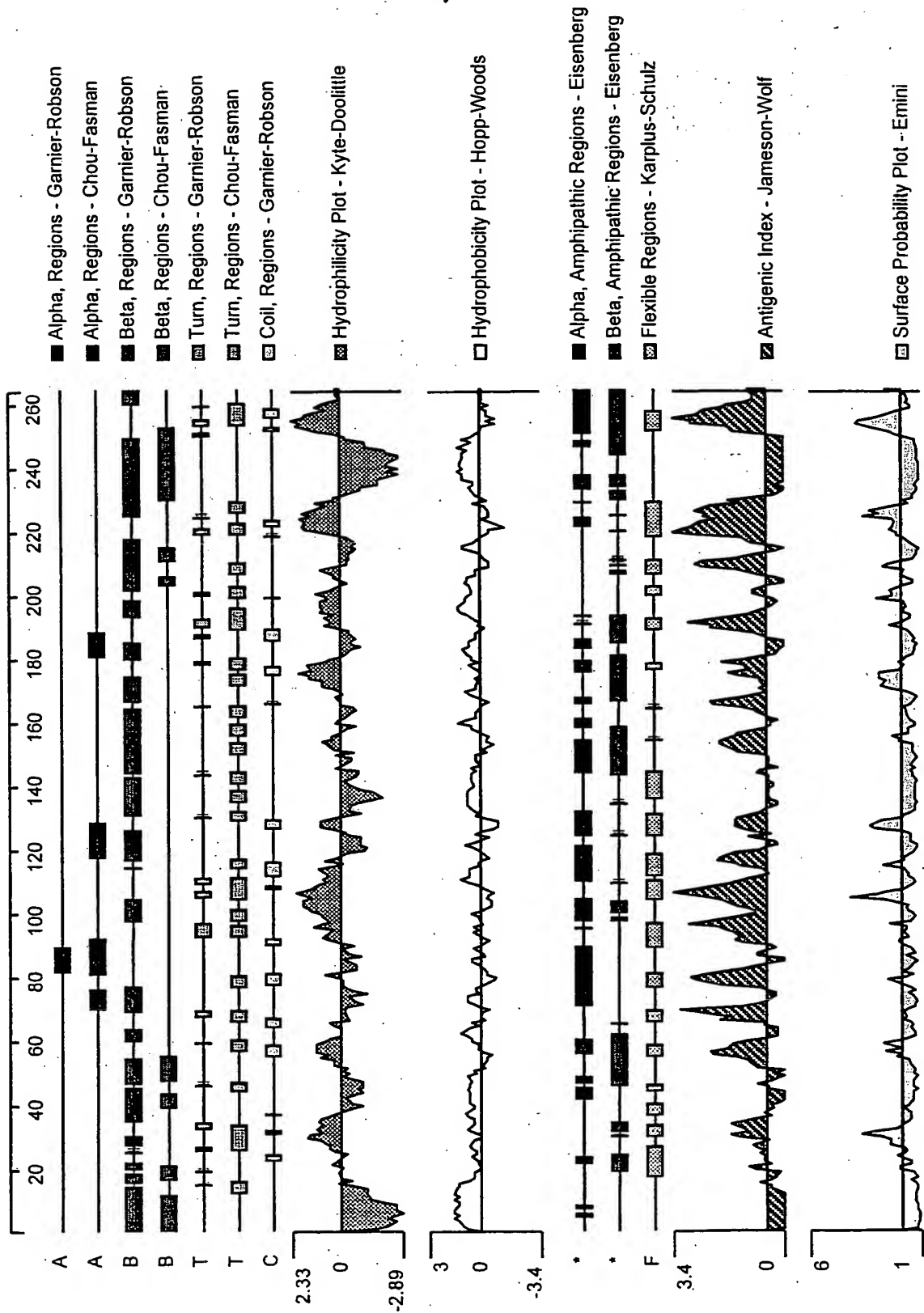


FIG. 6

9/21

FcR-III

1 GCAGGAATTCGGCAGCAGCACTGAGGGCTCATCCCTCTGCAGAGCGGGGTCACCG 60
61 GAAGGAGACGCCATGACGCCCCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGC 120
1 M T P A L T A L L C L G L S L G 16
121 CCCAGGACCCGCGTGCAGGCAGGGCCCTTCCCAAACCCACCCTCTGGGCTGAGCCAGGC 180
17 P R T R V Q A G P F P K P T L W A E P G 36
181 TCTGTGATCAGCTGGGGGAGCCCCGTGACCATCTGGTGTGAGGGAGCCTGGAGGCCAG 240
37 S V I S W G S P V T I W C Q G S L E A Q 56
241 GAGTACCAACTGGATAAAGAGGGAAGCCCAGAGCCCTTGGACAGAAATAACCCACTGGAA 300
57 E Y Q L D K E G S P E P L D R N N P L E 76
301 CCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACACAGCACCATGCAGGGAGATAC 360
77 P K N K A R F S I P S M T Q H H A G R Y 96
361 CGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCAGCGACCCCTGGAGCTGGTG 420
97 R C H Y Y S S A G W S E P S D P L E L V 116
421 ATGACAGGAGCCTATAGCAAACCCACCCTCTCAGCCCTGCCAGCCCTGTGGTGGCCTCA 480
117 M T G A Y S K P T L S A L P S P V V A S 136
481 GGGGGGAATATGACCCTCCGATGTGGCTCACAGAAGAGATATCACCATTTGTTCTGATG 540
137 G G N M T L R C G S Q K R Y H H F V L M 156
541 AAGGAAGGAGAACACCAGCTCCCCCGGACCCTGGA CTACAGCAGCTCCACAGTGGGGGG 600
157 K E G E H Q L P R T L D S Q Q L H S G G 176
601 TTCCAGGCCCTGTTCCTGTGGGCCCCGTGAACCCAGCCACAGGTGGAGGTTACATGC 660
177 F Q A L F P V G P V N P S H R W R F T C 196

FIG. 7A

10/21

FcR-III

661	TATTACTATTATATGAACACCCCCCGGGTGTGGTCCCACCCAGTGACCCCCTGGAGATT	720
197	Y Y Y Y M N T P R V W S H P S D P L E I	216
721	CTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCTGCAGGGCCCTGTCCTGGCC	780
217	L P S G V S R K P S L L T L Q G P V L A	236
781	CCTGGGCAGAGCCTGACCCTCCAGTGTGGCTCTGATGTCGGCTACGACAGATTTGTTCTG	840
237	P G Q S L T L Q C G S D V G Y D R F V L	256
841	TATAAGGAGGGGAACGTGACTTCCTCCAGCGCCCTGGCCAGCAGCCCCAGGCTGGGCTC	900
257	Y K E G E R D F L Q R P G Q Q P Q A G L	276
901	TCCCAGGCCAACTTCACCCCTGGGCCCTGTGAGCCCTCCAATGGGGGCCAGTACAGGTGC	960
277	S Q A N F T L G P V S P S N G G Q Y R C	296
961	TACGGTGCACACAACCTCTCCTCCGAGTGGTTCGGCCCCAGCGACCCCTGAACATCCTG	1020
297	Y G A H N L S S E W S A P S D P L N I L	316
1021	ATGGCAGGACAGATCTATGACACCGTCTCCCTGTCAGCACAGCCGGGCCCCACAGTGGCC	1080
317	M A G Q I Y D T V S L S A Q P G P T V A	336
1081	TCAGGAGAGAACGTGACCCTGCTGTGTGTCAGTCATGGTGGCAGTTTGACACTTTCCTTCTG	1140
337	S G E N V T L L C Q S W W Q F D T F L L	356
1141	ACCAAAGAAGGGGCAGCCATCCCCACTGCGTCTGAGATCAATGTACGGAGCTCATAAG	1200
357	T K E G A A H P P L R L R S M Y G A H K	376
1201	TACCAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCGGGGACCTACAGGTGC	1260
377	Y Q A E F P M S P V T S A H A G T Y R C	396
1261	TACGGCTCACGCAGCTCCAACCCCTACCTGCTGTCTACCCAGTGAGCCCCTGGAGCTC	1320
397	Y G S R S S N P Y L L S H P S E P L E L	416

FIG. 7B

11/21

FcR-III

1321	GTGGTCTCAGGACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCT	1380
417	V V S G H S G G S S L P P T G P P S T P	436
1381	GGTCTGGGAAGATACTGGAGGTTTTGATTGGGGTCTCGGTGGCCTTCGTCCTGCTGCTC	1440
437	G L G R Y L E V L I G V S V A F V L L L	456
1441	TTCCTCCTCCTTCTCCTCCTCCGACGTCAGCGTCACAGCAAACACAGGACATCTGAC	1500
457	F L L L F L L L R R Q R H S K H R T S D	476
1501	CAGAGAAAGACTGATTTCAGCGTCCTGCAGGGGCTGCGGAGACAGAGCCCAAGGACAGG	1560
477	Q R K T D F Q R P A G A A E T E P K D R	496
1561	GGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGAAGAAAACCTCTATGCTGCC	1620
497	G L L R R S S P A A D V Q E E N L Y A A	516
1621	GTGAAGGACACACAGTCTGAGGACGGGGTGGAGCTGGACAGTCAGAGCCCACACGATGAA	1680
517	V K D T Q S E D G V E L D S Q S P H D E	536
1681	GACCCCCACGCAGTGACGTATGCCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCC	1740
537	D P H A V T Y A P V K H S S P R R E M A	556
1741	TCTCCTCCTTCCCCACTGTCTGGGGAATTCCTGGACACAAAGGACAGACAGGCAGAAGAG	1800
557	S P P S P L S G E F L D T K D R Q A E E	576
1801	GACAGACAGATGGACACTGAGGCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCC	1860
577	D R Q M D T E A A A S E A S Q D V T Y A	596
1861	CAGCTGCACAGCTTGACCCTTAGACGGAAGGCAACTGAGCCTCCTCCATCCCAGGAGTTC	1920
597	Q L H S L T L R R K A T E P P P S Q E F	616
1921	GAGTCAGTCAGATCAGCATTGTGAGGCCCCATCTCTACAAAAAATAAAACCAGTCCGGCG	1980
617	E S V R S A L *	623

1981 TGGTGGCACA 1991

FIG. 7C

12/21

Percent Similarity: 69.697

Percent Identity: 53.788

HMPAP73.aa x FCg2RBos.aa

```
1 MTPALTALLCLGLSLGPRTRVQAGFPKPTLWAEPGSVISWGSPTIWCQ 50
  |.|.|.|||||:| ||.||||.||||:||||:|:|:|.|.||||:|
1 MAPTLPALLCLGLSVGLRTQVQAGTFPKPIIWAEPSSVVPLGSSVTILCQ 50

51 GSLEAQEYQLDKEGSPEPLDRNNPLEPKNKARFSIPSMTQHHAGRYRCHY 100
  |. :...: |:|...|:: : .|||:|.| |... ::|||:| .
51 GPPNTKSFSLNKEGDSTPWNHPSLEPWDKANFFISNVREQQAGRYHCSH 100

101 YSSAGWSEPSDPLELVMGTGAYSKPTLSALPSPVVASGGNMTLRCSQKRY 150
  : ...|||:|:|:|. .
101 FIGVNWSEPEPLDLLVAGEEP..... 122

151 HHFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGPVNPSHRWRFTCYYYY 200
122 ..... 122

201 MNTPRVWSHPSDPLEILPSGVSRKPSLLTLQGPVLAPGQSLTLQCGSDVG 250
122 ..... 122

251 YDRFVLYKEGERDFLQRPQGPQAGLSQANFTLGPVSPSNGGQYRCYGAH 300
122 ..... 122

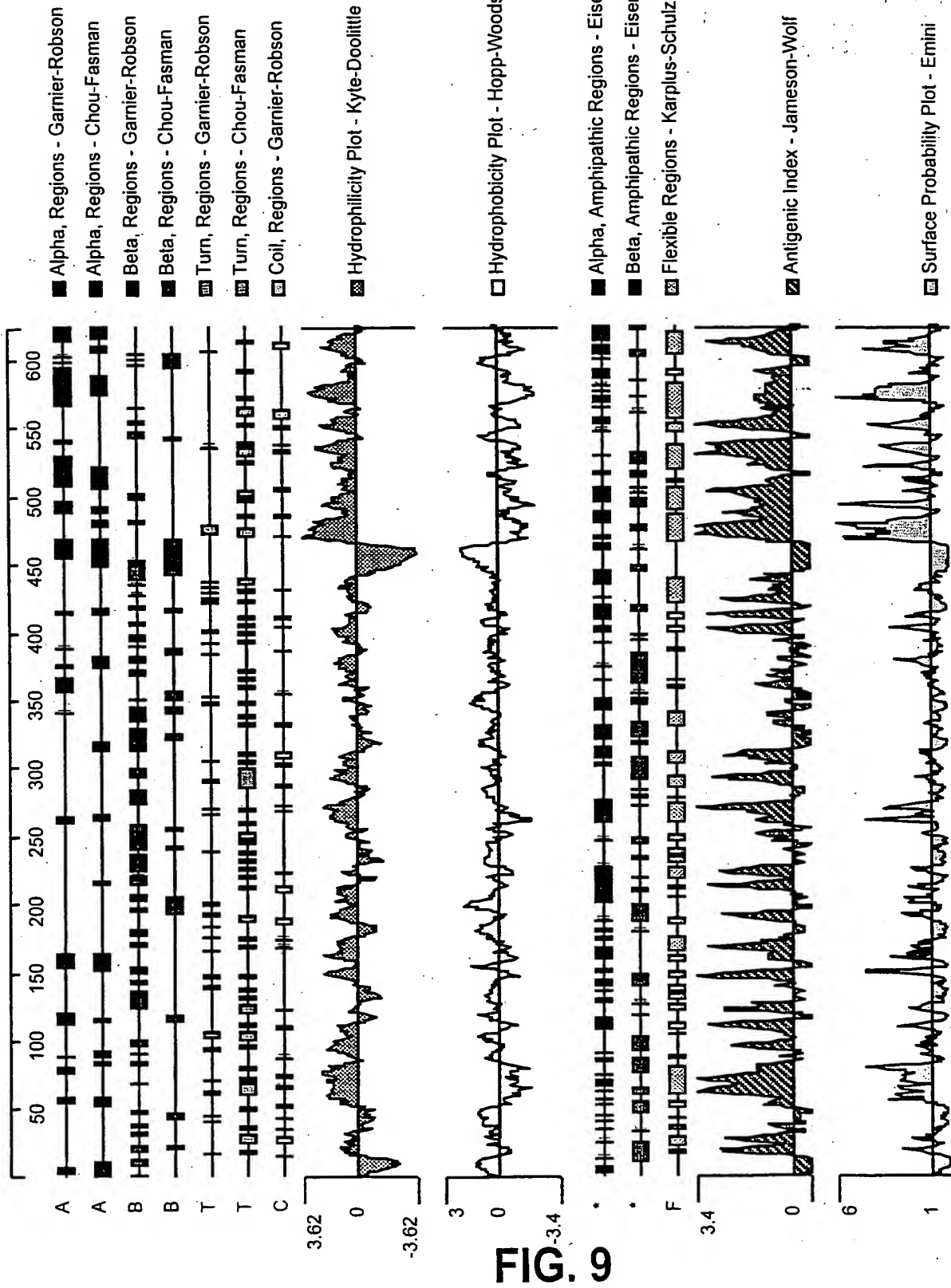
301 NLSSEWSAPSDPLNILMAGQIYDTVLSAQPGPTVASGENVTLLCQSWWQ 350
      ||.: | .||...|:|.||.|||||
123 .....AGRLRDRPSLSVRPSPSVAPGENVTLLCQSGNR 155

351 FDTFLLTKEGAHPPLRLRSMYGAHKYQAEFPMSPVTSAHAGTYRCYGSR 400
      |||||.|||||.||||| .. .||||.:|||||:||||| |
156 TDTFLLSKEGAHRPLRLRSQDQDGWYQAEFSLSPVTSAHGGTYRCYRSL 205

401 SSNPYLLSHPSEPLELVVSGHSGGSSLPPTGPPSTPGLGRYLEVLIGVSV 450
  |.|||||:|||||.|:|... :: || :::
206 STNPYLLSQPSEPLALLVADYT.....MQNLIRMGL 236

451 AFVLLLFLLLFLLLRRQRHSHKRTSDQR 478
  | :||:| ::| |: |: |.....
237 AASVLLLGLLCQARHDHGGAREAAARS 264
```

FIG. 8



14/21
FcR-IV

1	GGAATTCGGGAGGAGACGCCATGATCCCCACCTTCACGGCTCTGCTCTGCCTCGGGCTG	60
1	<u>M I P T F T A L L C L G L</u>	13
61	AGTCTGGGCCCCAGTACCCACATGCAGGCAGGGCCCTCCCCAAACCCACCCTCTGGGCT	120
14	<u>S L G</u> P S T H M Q A G P L P K P T L W A	33
121	GAGCCAGGCTCTGTGATCAGCTGGGGAACTCTGTGACCATCTGGTGTGAGGGGACCCTG	180
34	E P G S V I S W G N S V T I W C Q G T L	53
181	GAGGCTCGGGAGTACCGTCTGGATAAAGAGGAAAGCCCAGCACCCCTGGGACAGACAGAAC	240
54	E A R E Y R L D K E E S P A P W D R Q N	73
241	CCACTGGAGCCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGGACTATGCA	300
74	P L E P K N K A R F S I P S M T E D Y A	93
301	GGGAGATACCGCTGTTACTATCGCAGCCCTGTAGGCTGGTCACAGCCCAGTGACCCCTG	360
94	G R Y R C Y Y R S P V G W S Q P S D P L	113
361	GAGCTGGTGATGACAGGAGCCTACAGTAAACCCACCCTTTCAGCCCTGCCGAGTCCTCTT	420
114	E L V M T G A Y S K P T L S A L P S P L	133
421	GTGACCTCAGGAAAGAGCGTGACCCTGCTGTGTCAGTCACGGAGCCCAATGGACACTTTT	480
134	V T S G K S V T L L C Q S R S P M D T F	153
481	CTTCTGATCAAGGAGCGGGCAGCCCATCCCCTACTGCATCTGAGATCAGAGCACGGAGCT	540
154	L L I K E R A A H P L L H L R S E H G A	173
541	CAGCAGCACCAGGCTGAATCCCCATGAGTCCTGTGACCTCAGTGCACGGGGGACCTAC	600
174	Q Q H Q A E F P M S P V T S V H G G T Y	193
601	AGGTGCTTCAGCTCACACGGCTTCTCCCACTACCTGCTGTCACACCCAGTGACCCCTG	660
194	R C F S S H G F S H Y L L S H P S D P L	213
661	GAGTCATAGTCTCAGGATCCTTGGAGGGTCCCAGGCCCTCACCCACAAGGTCCGTCTCA	720
214	E L I V S G S L E G P R P S P T R S V S	233

FIG. 10A

15/21
Fcr-IV

721	ACAGCTGCAGGCCCTGAGGACCAGCCCCTCATGCCTACAGGGTCAGTCCCCACAGTGGT	780
234	T A A G P E D Q P L M P T G S V P H S G	253
781	CTGAGAAGGCACTGGGAGGTACTGATCGGGGTCTTGGTGGTCTCCATCCTGCTTCTCTCC	840
254	L R R H W E V L I G V L V V S I L L L S	273
841	CTCCTCCTCTTCTCCTCCTCCAACACTGGCGTCAGGGAAAACAGGACATTGGCCCAG	900
274	L L L F L L L Q H W R Q G K H R T L A Q	293
901	AGACAGGCTGATTTCCAACGTCCTCCAGGGGTGCCGAGCCAGAGCCCAAGGACGGGGGC	960
294	R Q A D F Q R P P G A A E P E P K D G G	313
961	CTACAGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGGAGAAACTTCTGTGCTGCCGTG	1020
314	L Q R R S S P A A D V Q G E N F C A A V	333
1021	AAGGACACACAGCCTGAGGACGGGGTGGAAATGGACACTCGGCAGAGCCCACACGATGAA	1080
334	K D T Q P E D G V E M D T R Q S P H D E	353
1081	GACCCCCAGGCAGTGACGTATGCCAAGGTGAAACACTCCAGACCTAGGAGAGAAATGGCC	1140
354	D P Q A V T Y A K V K H S R P R R E M A	373
1141	TCTCCTCCCTCCCCACTGTCTGGGGAATTCCTGGACACAAAGGACAGACAGGCAGAAGAG	1200
374	S P P S P L S G E F L D T K D R Q A E E	394
1201	GACAGACAGATGGACACTGAGGCTGCTGCATCTGAAGCCCCCAGGATGTGACTACGCCC	1260
395	D R Q M D T E A A A S E A P Q D V T T P	413
1261	GGCTGCACAGCTTTACCCTCAGACAGAAGGCAACTGAGCCTCCTCCATCCCAGGAAGGGG	1320
414	G C T A L P S D R R Q L S L L H P R K G	433
1321	CCTCTCCAGCTGAGCCCAGTGTCTATGCCACTCTGGCCATCCACTAATCCAGGGGGGACC	1380
434	P L Q L S P V S M P L W P S T N P G G T	453
1381	CAGACCCACAAGCCATGGAGACTCAGGACCCAGAGGCATGGAAGCTGCCTCCAGTAG	1440
454	Q T P Q A M E T Q D P R R H G S C L Q *	472
1441	ACATCACTGAACCCAGCCAGCCAGACCCCTGACACAGACCACTAGAAGATTCCGGGAA	1500
1501	CGTGGGAGTCACCTGATTCTGCAAAGATAAATAATATCCCTGCATTATC	1550

FIG. 10B

16/21

Percent Similarity: 67.969 Percent Identity: 50.781

HMSHH46new.aa x FCg2RBos.aa

```
1 MIPTFTALLCLGLSLGPSTHMQAGPLPKPTLWAEPGSVISWGNVSVTIWCQ 50
  | |:::|||||||:| .|::|||.:|||.:|||:|:|:|.||||:|
1 MAPTLPALCLGLSVGLRTQVQAGTFPKPIIWAEPSSVVPLGSSVTILCQ 50

51 GTLEAREYRLDKEESPAPWDRQNPLEPKNKARFSIPSMTEYAGRYRCYY 100
  |. :.:.:|:|:..|: : .|||.:|||. |.: |: |||:| .
51 GPNTKSFSLNKEGDSTPWNHPSLEPWDKANFFISNVREQQAGRYHCSH 100

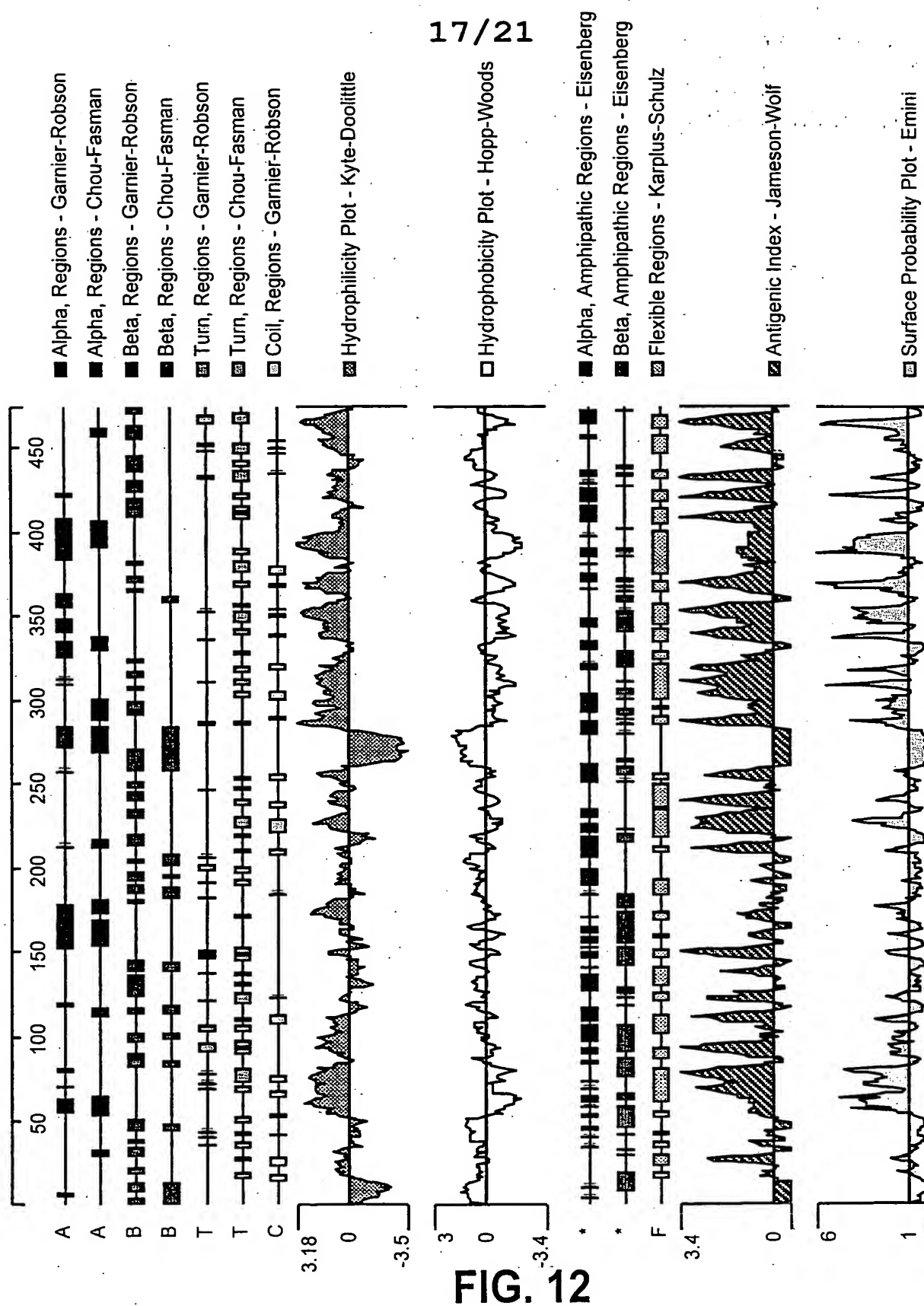
101 RSPVGWSQPSDPLELVMTGAYS.....KPTLSALPSPLVTSGKSVTLLC 144
   .|.||:|:|:|:|:|. . :|.||. ||| |..|..||||
101 FIGVNWSEPEPLDLLVAGEEPAGRLRDRPSLSVRPSPSVAPGENVTLLC 150

145 QSRSPMDTFLLIKERAAHPLLHLRSEHGAQQHQAEFPMSPVTSVHGGTYR 194
  || .. ||||| || |||. |:|:|:.... .|||:|:|:|:|:|:|
151 QSGNRTDTFLLSKEGAHRPLRLRSQDQDGWYQAEFSLSPVTSAHGGTYR 200

195 CFSSHGFSHYLLSHPSDPLELIVSGSLEGPRPSPTRSVSTAAGPEDQPLM 244
  |:|:|: ..|||:|:|:|:|:| |: . | |:
201 CYRSLSTNPYLLSQPSEPLALLV.....ADYTMQNLI 232

245 PTGSVPHSGLRRHWEVLIGVLVVSILLLSLLLFLLLQHWROGKHRTLAQR 294
  . | |..|:| | :|: |::| :.
233 RMG.....LAASVLLLLGILL.....CQARHDHGGAR 259
295 QAD 297
   :|.
260 EAA 262
```

FIG. 11



18/21

FcR-V

1	GCAGGAATTCGGCACGAGCAGAGCAGGGCAGTGGGAGGAGACGCCATGACCCCATCCTC	60
1	<u>M T P I L</u>	5
61	ACGGTCCTGATCTGTCTCGGGCTGAGTCTGGGCCCCAGGACCCACGTGCAGGCAGGGCAC	120
6	<u>T V L I C L G L S L G P R T H V Q A G H</u>	25
121	CTCCCCAAGCCCACCCTCTGGGCTGAGCCAGGCTCTGTGATCATCCAGGGAAGTCCTGTG	180
26	L P K P T L W A E P G S V I I Q G S P V	45
181	ACCCTCAGGTGTCAGGGGAGCCTTCAGGCTGAGGAGTACCATCTATATAGGGAAAACAAA	240
46	T L R C Q G S L Q A E E Y H L Y R E N K	65
241	TCAGCATCCTGGGTTAGACGGATACAAGAGCCTGGGAAGAATGGCCAGTTCCTCATCCCA	300
66	S A S W V R R I Q E P G K N G Q F P I P	85
301	TCCATCACCTGGGAACACGCAGGGCGGTATCACTGTCAGTACTACAGCCACAATCACTCA	360
86	S I T W E H A G R Y H C Q Y Y S H N H S	105
361	TCAGAGTACAGTGACCCCCTGGAGCTGGTGGTGACAGGAGCCTACAGCAAACCCACCCTC	420
106	S E Y S D P L E L V V T G A Y S K P T L	125
421	TCAGCTCTGCCAGCCCTGTGGTGACCTTAGGAGGGAACGTGACCCTCCAGTGTGTCTCA	480
126	S A L P S P V V T L G G N V T L Q C V S	145
481	CAGGTGGCATTGACGGCTTCATTCTGTGTAAGGAAGGAGAAGATGAACACCCACAACGC	540
146	Q V A F D G F I L C K E G E D E H P Q R	165
541	CTGAACCTCCCATTCCTATGCCCGTGGGTGGTCTGGGCCATCTTCTCCGTGGGCCCCGTG	600
166	L N S H S H A R G W S W A I F S V G P V	185
601	AGCCCGAGTCGCAGGTGGTTCGTACAGGTGCTATGCTTATGACTCGAAGTCTCCCTATGTG	660
186	S P S R R W S Y R C Y A Y D S N S P Y V	205
661	TGGTCTCTACCCAGTGATCTCCTGGAGCTCCTGGTCCCAGGTGTTTCTAAGAAGCCATCA	720
206	W S L P S D L L E L L V P G V S K K P S	225
721	CTCTCAGTGCAGCCAGGTCTATGGTGGCCCCCTGGGAGAGCCTGACCCTCCAGTGTGTC	780
226	L S V Q P G P M V A P G E S L T L Q C V	245
781	TCTGATGTCGGCTACGACAGATTGTTCTGTATAAGGAGGAGAACGTGACTTCCTCCAG	840
246	S D V G Y D R F V L Y K E G E R D F L Q	265

FIG. 13A

19/21

FcR-V

841	CGCCCTGGTTGGCAGCCCCAGGCTGGGCTCTCCAGGCCAACTTCACCCTGGGCCCTGTG	900
266	R P G W Q P Q A G L S Q A N F T L G P V	285
901	AGCCCTCCACGGGGGCCAGTACAGATGCTACAGTGCACACAACCTCTCCTCCGAGTGG	960
286	S P S H G G Q Y R C Y S A H N L S S E W	305
961	TCGGCCCCAGTGACCCCTGGACATCCTGATCACAGGACAGTTCTATGACAGACCCTCT	1020
306	S A P S D P L D I L I T G Q F Y D R P S	325
1021	CTCTCGGTGCAGCCGGTCCCCACAGTAGCCCCAGGAAAGAACGTGACCCTGCTGTGTGAG	1080
326	L S V Q P V P T V A P G K N V T L L C Q	345
1081	TCACGGGGCAGTTCACACTTTCCTTCTGACCAAGGAGGGGGCAGGCCATCCCCACTG	1140
346	S R G Q F H T F L L T K E G A G H P P L	365
1141	CATCTGAGATCAGAGCACCAGCTCAGCAGAACCAGGCTGAATTCCGCATGGGTCTGTG	1200
366	H L R S E H Q A Q Q N Q A E F R M G P V	385
1201	ACCTCAGCCCACGTGGGGACCTACAGATGCTACAGCTCACTCAGCTCCAACCCCTACCTG	1260
386	T S A H V G T Y R C Y S S L S S N P Y L	405
1261	CTGTCTCTCCCAGTGACCCCTGGAGCTCGTGGTCTCAGCATCCCTAGGCCAACACCCC	1320
406	L S L P S D P L E L V V S A S L G Q H P	425
1321	CAGGATTACACAGTGGAGAATCTCATCCGCATGGGTGTGGCTGGCTTGGTCTGGTGGTC	1380
426	Q D Y T V E N L I R M G V A G L V L V V	445
1381	CTCGGGATTCTGCTATTTGAGGCTCAGCACAGCCAGAGAAGCCTACAAGATGCAGCCGGG	1440
446	L G I L L F E A Q H S Q R S L Q D A A G	465
1441	AGTGAACAGCAGAGAGGACAATGCATCCTTCAGCGTGGTGGAGCCTCAGGGACAGATCTG	1500
466	S E Q Q R G Q C I L Q R G G A S G T D L	485
1501	ATGATCCCAGGAGGCTCTGGAGGACAATCTAGGACCTACATTATCTGGACTGTATGCTGG	1560
486	M I P G G S G G Q S R T Y I I W T V C W	505
1561	TCATTTCTAGAGACAGCAATCAATATTTGAGTGTAAAGGAACTGTCTGGGGTGATTCTTA	1620
506	S F L E T A I N I *	514
1621	GAAGATCATTAACTGTGGTACATTTTTTTGTCTATG	1657

FIG. 13B

Percent Similarity: 70.722 Percent Identity: 55.513
HMAAB68.aa x FCg2RBos.aa

FIG. 14

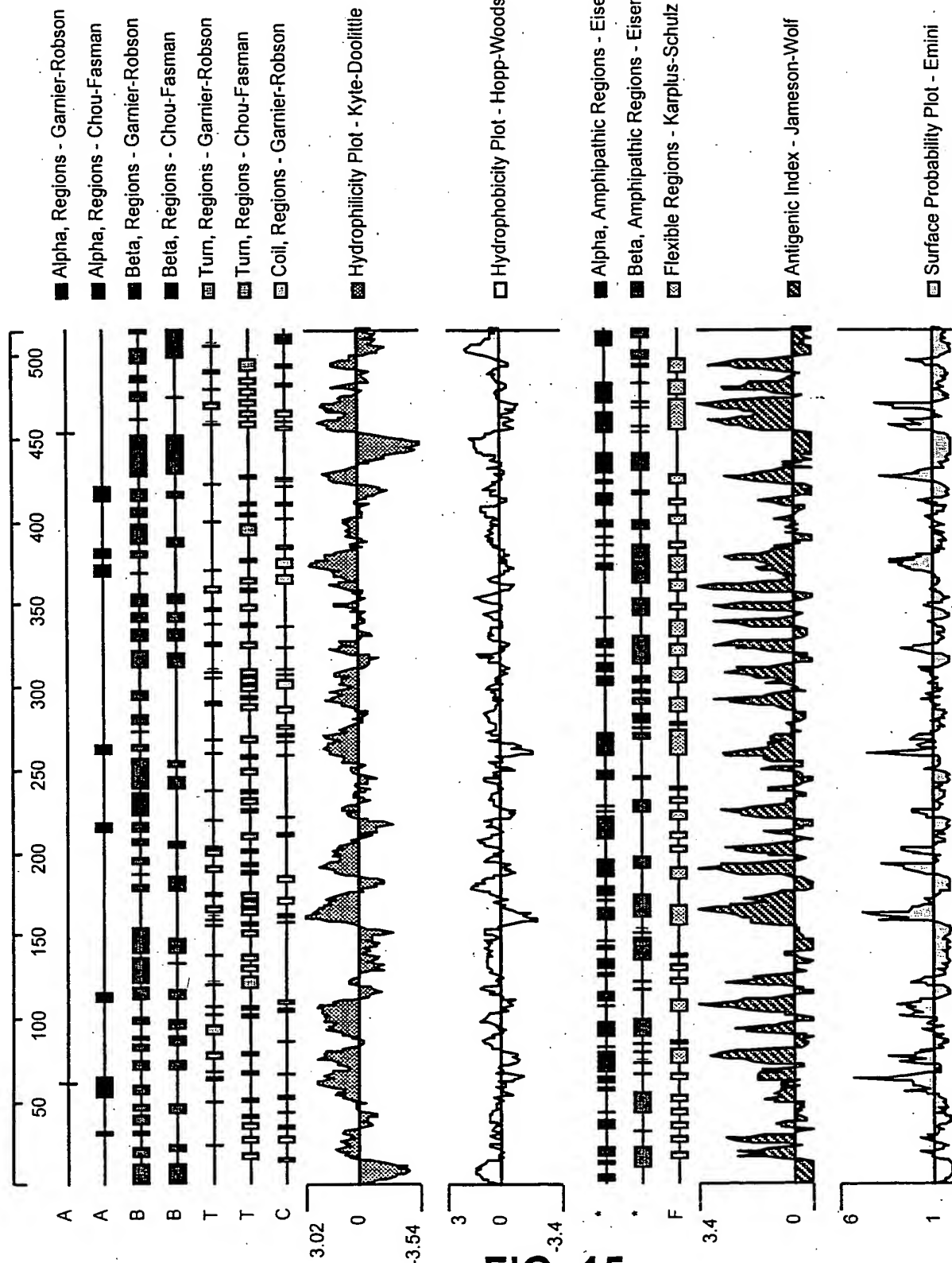


FIG. 15